

PATENT

Attorney Docket No.: 6056-279

IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

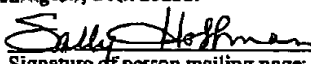
In re: Patent application of Clara Fronticelli :
Serial No.: 09/787,216 : Group Art Unit:
Filed: March 14, 2001 : Examiner:
For: Polymeric Hemoglobins Mutants :

STATEMENT PURSUANT TO 37 CFR § 1.8259(a)(b)

Commissioner for Patents
Box PCT
Washington, D.C. 20231

Sir:

The Substitute Sequence Listing filed herewith includes no new matter. The content of the substitute Sequence Listing in computer readable form is the same as the substitute paper copy of the Sequence Listing submitted herewith.

<p align="center">CERTIFICATE OF MAILING UNDER 37 C.F.R. 1.10</p> <p>EXPRESS MAIL Mailing Label Number: ET324713790US</p> <p>Date of Deposit: <u>5/30/02</u></p> <p>I hereby certify that this correspondence, along with any paper referred to as being attached or enclosed, and/or fee, is being deposited with the United States Postal Service, "EXPRESS MAIL-POST OFFICE TO ADDRESSEE" service under 37 CFR 1.10, on the date indicated above, and addressed to: Commissioner for Patents, Washington, D.C. 20231.</p> <p> Signature of person mailing page:</p> <p><u>Sally Hoffman</u> Type or print name of person</p>
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Respectfully submitted,

CLARA FRONTICELLI

BY 

DANIEL A. MONACO
Reg. No. 30,480
DRINKER, BIDDLE & REATH, LLP.
One Logan Square
18th and Cherry Streets
Philadelphia, PA 19103-6996
(215) 988-3312
(215) 988-2757 – fax
Attorney for the Applicant

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RAW SEQUENCE LISTING

DATE: 12/09/2002

PATENT APPLICATION: US/09/787,216A

TIME: 11:48:47

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1 <110> APPLICANT: Fronticelli, Clara
2 <120> TITLE OF INVENTION: POLYMERIC HEMOGLOBIN MUTANTS
3 <130> FILE REFERENCE: 6056-279 PC
4 <140> CURRENT APPLICATION NUMBER: 09/787,216A
5 <141> CURRENT FILING DATE: 2002-09-20
7 <150> PRIOR APPLICATION NUMBER: PCT/US99/22756
8 <151> PRIOR FILING DATE: 1999-09-30
10 <150> PRIOR APPLICATION NUMBER: 60/102,640
11 <151> PRIOR FILING DATE: 1998-10-01
12 <160> NUMBER OF SEQ ID NOS: 12
13 <170> SOFTWARE: PatentIn Ver. 2.0
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18 <213> ORGANISM: Human
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21      gatgaagttg gtggtgaggc cctgggcagg ctgctggtgg tctacccttg gaccagagg 120
22      ttctttgagt cctttgggga tctgtccact cctgatgctg ttatgggcaa ccctaaggtg 180
23      aaggctcatg gcaagaaagt gctcggtgcc tttagtgatg gcctggctca cctggacaac 240
24      ctcaagggca cctttgccac actgagttag ctgcatgctg acaagctgca cgtggatcct 300
25      gagaacttca ggctcctggg caacgtgctg gtctgtgtgc tggcccatca ctttggcaaa 360
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42      gagaacttca ggctcctggg caacgtgctg gtcggtgtgc tggcccatca ctttggcaaa 360
43      gaattcacc caccagtga ggctgcctat cagaaagtgg tggctggtgt ggctaatacc 420
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46 <210> SEQ ID NO: 3
47 <211> LENGTH: 146
48 <212> TYPE: PRT

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RAW SEQUENCE LISTING

DATE: 12/09/2002

PATENT APPLICATION: US/09/787,216A

TIME: 11:48:47

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53   Lys Val Asn Val Asp Glu Val Gly Gly Glu Ala Leu Gly Arg Leu Leu
54           20           25           30
55   Val Val Tyr Pro Trp Thr Gln Arg Phe Phe Glu Ser Phe Gly Asp Leu
56           35           40           45
57   Ser Thr Pro Asp Ala Val Met Gly Asn Pro Lys Val Lys Ala His Gly
58     50           55           60
59   Lys Lys Val Leu Gly Ala Phe Ser Asp Gly Leu Ala His Leu Asp Asn
60     65           70           75           80
61   Leu Lys Gly Thr Phe Ala Thr Leu Ser Glu Leu His Cys Asp Lys Leu
62           85           90           95
63   His Val Asp Pro Glu Asn Phe Arg Leu Leu Gly Asn Val Leu Val Cys
64           100          105          110
65   Val Leu Ala His His Phe Gly Lys Glu Phe Thr Pro Pro Val Gln Ala
66           115          120          125
67   Ala Tyr Gln Lys Val Val Ala Gly Val Ala Asn Ala Leu Ala His Lys
68     130          135          140
69   Tyr His
70     145
72 <210> SEQ ID NO: 4
73 <211> LENGTH: 146
74 <212> TYPE: PRT
75 <213> ORGANISM: Artificial Sequence
76 <220> FEATURE:
77 <223> OTHER INFORMATION: Description of Artificial Sequence: Mutant of
78   human beta-globin
79 <400> SEQUENCE: 4
80   Val His Leu Thr Pro Glu Glu Lys Cys Ala Val Thr Ala Leu Trp Gly
81     1           5           10           15
82   Lys Val Asn Val Asp Glu Val Gly Gly Glu Ala Leu Gly Arg Leu Leu
83           20           25           30
84   Val Val Tyr Pro Trp Thr Gln Arg Phe Phe Glu Ser Phe Gly Asp Leu
85           35           40           45
86   Ser Thr Pro Asp Ala Val Met Gly Asn Pro Lys Val Lys Ala His Gly
87     50           55           60
88   Lys Lys Val Leu Gly Ala Phe Ser Asp Gly Leu Ala His Leu Asp Asn
89     65           70           75           80
90   Leu Lys Gly Thr Phe Ala Thr Leu Ser Glu Leu His Ala Asp Lys Leu
91           85           90           95
92   His Val Asp Pro Glu Asn Phe Arg Leu Leu Gly Asn Val Leu Val Gly
93           100          105          110
94   Val Leu Ala His His Phe Gly Lys Glu Phe Thr Pro Pro Val Gln Ala
95           115          120          125
96   Ala Tyr Gln Lys Val Val Ala Gly Val Ala Asn Ala Leu Ala His Lys
97     130          135          140
98   Tyr His

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108     Val Gly Ala His Ala Gly Glu Tyr Gly Ala Glu Ala Leu Glu Arg Met
109             20             25             30
110     Phe Leu Ser Phe Pro Thr Thr Lys Thr Tyr Phe Pro His Phe Asp Leu
111             35             40             45
112     Ser His Gly Ser Ala Gln Val Lys Gly His Gly Lys Lys Val Ala Asp
113             50             55             60
114     Ala Leu Thr Asn Ala Val Ala His Val Asp Asp Met Pro Asn Ala Leu
115             65             70             75             80
116     Ser Ala Leu Ser Asp Leu His Ala His Lys Leu Arg Val Asp Pro Val
117             85             90             95
118     Asn Phe Lys Leu Leu Ser His Cys Leu Leu Val Thr Leu Ala Ala His
119             100            105            110
120     Leu Pro Ala Glu Phe Thr Pro Ala Val His Ala Ser Leu Asp Lys Phe
121             115            120            125
122     Leu Ala Ser Val Ser Thr Val Leu Thr Ser Lys Tyr Arg
123             130            135            140
125 <210> SEQ ID NO: 6
126 <211> LENGTH: 141
127 <212> TYPE: PRT
128 <213> ORGANISM: Artificial Sequence
129 <220> FEATURE:
130 <223> OTHER INFORMATION: Description of Artificial Sequence: Mutant of
131     human alpha-globin
132 <400> SEQUENCE: 6
133     Val Leu Ser Pro Ala Asp Lys Thr Asn Val Lys Ala Ala Trp Gly Lys
134         1             5             10             15
135     Val Gly Ala His Ala Gly Glu Tyr Gly Ala Glu Ala Leu Glu Arg Met
136             20             25             30
137     Phe Leu Ser Phe Pro Thr Thr Lys Thr Tyr Phe Pro His Phe Asp Leu
138             35             40             45
139     Ser His Gly Ser Ala Gln Val Lys Gly His Gly Lys Lys Val Ala Asp
140             50             55             60
141     Ala Leu Thr Asn Ala Val Ala His Val Asp Asp Met Pro Asn Ala Leu
142             65             70             75             80
143     Ser Ala Leu Ser Asp Leu His Ala His Lys Leu Arg Val Asp Pro Val
144             85             90             95
145     Asn Phe Lys Leu Leu Ser His Ser Leu Leu Val Thr Leu Ala Ala His
146             100            105            110
147     Leu Pro Ala Glu Phe Thr Pro Ala Val His Ala Ser Leu Asp Lys Phe
148             115            120            125
149     Leu Ala Ser Val Ser Thr Val Leu Thr Ser Lys Tyr Arg

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155 <213> ORGANISM: Artificial Sequence
156 <220> FEATURE:
157 <223> OTHER INFORMATION: Description of Artificial Sequence: Mutant of
158     human alpha-globin
159 <400> SEQUENCE: 7
160     gtgctgtctc ctgccgacaa gaccaacgtc aaggccgcct ggggcaaggt tggcgcgcac 60
161     gctggcgagt atggtgcgga ggccctggag aggatgttcc tgtccctccc caccaccaag 120
162     acctacttcc cgcacttcga cctgagccac ggctctgccc aggttaaggg ccacggcaag 180
163     aagggtggccg acgcgctgac caacgccgtg gcgcacgtgg acgacatgcc caacgcgctg 240
164     tccgccctga gcgacctgca cgcgacaaag cttcgggtgg acccgggtcaa cttcaagctc 300
165     ctaagccact ccctgctggt gaccctggcc gccacctcc ccgccgagtt caccctgcg 360
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167     cgt
169 <210> SEQ ID NO: 8
170 <211> LENGTH: 4
171 <212> TYPE: PRT
172 <213> ORGANISM: Artificial Sequence
173 <220> FEATURE:
174 <223> OTHER INFORMATION: Description of Artificial Sequence: Factor Xa
175     recognition sequence
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177     Ile Glu Gly Arg
178     1
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181 <211> LENGTH: 27
182 <212> TYPE: DNA
183 <213> ORGANISM: Artificial Sequence
184 <220> FEATURE:
185 <223> OTHER INFORMATION: Description of Artificial Sequence: Mutagenizing
186     oligonucleotide for human beta-globin Ser9- Cys
187     mutation
188 <400> SEQUENCE: 9
189     ggcagtaacg gcgcacttct cctcagg
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192 <211> LENGTH: 27
193 <212> TYPE: DNA
194 <213> ORGANISM: Artificial Sequence
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198     mutation
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200     tgcagcttgt cagcatgcag ctcactc
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203 <211> LENGTH: 18

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RAW SEQUENCE LISTING

DATE: 12/09/2002

PATENT APPLICATION: US/09/787,216A

TIME: 11:48:48

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209     mutation
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216 <213> ORGANISM: Human
217 <400> SEQUENCE: 12
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219     gctggcgagt atggtgcgga ggccctggag aggatgttcc tgtccttccc caccaccaag 120
220     acctacttcc cgcacttcga cctgagccac ggctctgccc aggttaaggg ccacggcaag 180
221     aaggtggcgc acgcgctgac caacgccgtg gcgcacgtgg acgacatgcc caacgcgctg 240
222     tccgccctga gcgacctgca cgcgcacaag cttcgggtgg acccggtcaa cttcaagctc 300
223     ctaagccact gcctgctggg gaccctggcc gccacactcc ccgccgagtt caccctgcg 360
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VERIFICATION SUMMARY

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PATENT APPLICATION: US/09/787,216A

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